

09/596,746.



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Raymond J. Dattwyler, Gerald Seinost, Daniel Dykhuizen, Benjamin J. Luft,  
Maria J.C. Gomes-Solecki

C g C  
EME

Issued: June 13, 2006

Patent No.: 7,060,281 B1

Title: GROUPS OF BORRELIA BURGDORFERI AND BORRELIA AFZELII  
THAT CAUSE LYME DISEASE IN HUMANS

CERTIFICATE OF MAILING OR TRANSMISSION	
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6/22/07	Katie Norris
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Katie Norris	
Typed or printed name of person signing certificate	

**REQUEST FOR CERTIFICATE OF CORRECTION**

Office of Publications  
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Alexandria, VA 22313-1450

Certificate  
JUN 28 2007  
of Correction

Sir:

Pursuant to 35 U.S.C. § 254, we hereby request a Certificate of Correction be issued for the above-referenced U.S. Letters Patent for the following reasons:

SEQ ID NOS. 53-86 were not included in the issued patent, even though they were properly entered in a Substitute Sequence Listing filed on September 22, 2005. Certain of the claims recite SEQ ID NOS that are not in the published patent, which will be confusing for the public.

Since the errors were made by the U.S. Patent and Trademark Office and not by Patentees or Patentee's Attorney/Agent, it is understood that there are no additional fees for the requested Certificate of Correction. A Certificate of Correction is enclosed herewith.

Respectfully submitted,

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Elizabeth W. Mata  
Registration No.: 38,236  
Telephone: (978) 341-0036  
Facsimile: (978) 341-0136

Concord, MA 01742-9133

Dated: June 22, 2007

# UNITED STATES PATENT AND TRADEMARK OFFICE

## CERTIFICATE OF CORRECTION

PATENT NO. : 7,060,281 B1  
 DATED : June 13, 2006  
 INVENTOR(S) : Raymond J. Dattwyler, Gerald Seinost, Daniel  
 Dykhuizen, Benjamin J. Luft, Maria J.C. Gomes-Solecki

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

**At Column 45, Insert SEQ ID NOS. 53-86 after SEQ ID NO: 52**

<210> 53

<211> 1137

<212> DNA

<213> ospC Chimera

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<221> CDS

<222> (1)... (1137)

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35 40 45	

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192
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 Concord, Massachusetts 01742-9133

PATENT NO. 7,060,281 B1

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 @ 50¢ per page





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225 230 235 240

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cct gtt gtg gca gaa agt cca aaa aaa cct taa	1137
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Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
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Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
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Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
      20                      25                      30

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      35                      40                      45

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130 135 140	
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Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser	
275 280 285	

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 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys  
 50 55 60  
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser  
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Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Leu Gly Lys Leu
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Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
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Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
      180                    185                    190
Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
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Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
      210                    215                    220
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
225      230                    235                    240
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Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
      260                    265                    270
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
      275                    280                    285
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
      290                    295                    300
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
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Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
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7,060,281 B1

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Pro  
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Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
      355              360              365

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1152
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Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
                      165                      170                      175
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
                      180                      185                      190
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
                      195                      200                      205
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
210                      215                      220
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
225                      230                      235                      240
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
                      245                      250                      255
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
                      260                      265                      270
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
275                      280                      285
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
290                      295                      300
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
305                      310                      315                      320
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
                      325                      330                      335
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
                      340                      345                      350
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
355                      360                      365
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
370                      375                      380
Lys Pro
385

```

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Concord, Massachusetts 01742-9133

<210> 59  
 <211> 1197  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1197)

<400> 59  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480

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Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145	150 155 160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165	170 175
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180	185 190
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195	200 205
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat	672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp	
210	215 220
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat	720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
225	230 235 240
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc	768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
245	250 255
gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct	816
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala	
260	265 270
aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag	864
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu	
275	280 285
gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac	912
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn	
290	295 300
tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag	960
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys	
305	310 315 320
gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa	1008
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys	
325	330 335

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```

tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
      340              345              350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
      355              360              365

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
      370              375              380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
      385              390              395

```

<210> 60  
 <211> 399  
 <212> PRT  
 <213> ospC Chimera

```

<400> 60
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1              5              10              15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20              25              30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35              40              45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50              55              60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
      65              70              75              80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
      85              90              95
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
      100             105             110
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
      115             120             125
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
      130             135             140
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
      145             150             155             160
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
      165             170             175
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
      180             185             190

```

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021005

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```

Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
    195                200                205
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
    210                215                220
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
    225                230                235                240

Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
    245                250                255
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala
    260                265                270
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu
    275                280                285
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn
    290                295                300
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys
    305                310                315                320
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys
    325                330                335
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
    340                345                350
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
    355                360                365
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
    370                375                380
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
    385                390                395

```

```

<210> 61
<211> 1196
<212> DNA
<213> ospC Chimera

```

```

<220>
<221> CDS
<222> (1)...(1196)

```

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<400> 61
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1                5                10                15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa   96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
    20                25                30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65 70 75 80	
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp	
85 90 95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100 105 110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115 120 125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat	672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp	
210 215 220	

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021005

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```

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
225                230                235                240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg 768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
                245                250                255

gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct 816
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
                260                265                270

act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc 864
Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val
                275                280                285

gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca 912
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser
                290                295                300

aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta 960
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu
305                310                315                320

aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa 1008
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys
                325                330                335

aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat 1056
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp
                340                345                350

gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag 1104
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys
                355                360                365

ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca 1152
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala
                370                375                380

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac 1196
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385                390                395

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021005

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530 Virginia Road, P.O. Box 9133

Concord, Massachusetts 01742-9133

<210> 62  
 <211> 398  
 <212> PRT  
 <213> ospC Chimera

<400> 62  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
 210 215 220  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 225 230 235 240  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
 245 250 255  
 Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala  
 260 265 270  
 Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val  
 275 280 285  
 Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 290 295 300  
 Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu  
 305 310 315 320

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 Concord, Massachusetts 01742-9133

```

Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys
      325                      330                      335

Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp
      340                      345                      350
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys
      355                      360                      365
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala
      370                      375                      380
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
      385                      390                      395

```

```

<210> 63
<211> 1185
<212> DNA
<213> ospC Chimera

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```

<220>
<221> CDS
<222> (1)...(1185)

```

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<400> 63
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1                      5                      10                      15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa   96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20                      25                      30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt.aaa ggg cct   144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35                      40                      45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta   192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50                      55                      60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt   240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
      65                      70                      75                      80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta"gat aat   288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
      85                      90                      95

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100 105 110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115 120 125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130 135 140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145 150 155 160	
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165 170 175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	
agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser	
210 215 220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245 250 255	
gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt	816
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly	
260 265 270	
aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac	864

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021005

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 Concord, Massachusetts 01742-9133

```

Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn
    275                      280                      285

gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa    912
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys
    290                      295                      300

aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa    960
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu
    305                      310                      315                      320

aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa    1008
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu
    325                      330                      335

cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa    1056
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys
    340                      345                      350

gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt    1104
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu
    355                      360                      365

gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag    1152
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu
    370                      375                      380

atg ctt act aat tca gtt aaa gag ctt aca agc                            1185
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
    385                      390                      395

```

```

<210> 64
<211> 395
<212> PRT
<213> ospC Chimera

```

```

<400> 64
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1                      5                      10                      15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
    20                      25                      30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
    35                      40                      45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
    50                      55                      60

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021005  
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```

Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65              70              75              80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85              90              95
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100            105            110
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115            120            125
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130            135            140
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145            150            155            160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165            170            175
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180            185            190
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195            200            205
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
210            215            220
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225            230            235            240
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
245            250            255
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly
260            265            270
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn
275            280            285
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys
290            295            300
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu
305            310            315            320
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu
325            330            335
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys
340            345            350
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu
355            360            365
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu
370            375            380
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
385            390            395

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7,060,281 B1

021005

Hamilton, Brook, Smith & Reynolds, P.C.  
530 Virginia Road, P.O. Box 9133  
Concord, Massachusetts 01742-9133

<210> 65  
 <211> 1184  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1184)

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<400> 65
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt      48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1              5              10              15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa      96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
          20              25              30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct     144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35              40              45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta     192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50              55              60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt     240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
      65              70              75              80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat     288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
          85              90              95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca     336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
          100              105              110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta     384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
          115              120              125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act     432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
          130              135              140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat     480

```

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 Concord, Massachusetts 01742-9133

Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145	150 155 160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
	165 170 175
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
	180 185 190
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
	195 200 205
agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser	
	210 215 220
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
	225 230 235 240
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
	245 250 255
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att	816
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile	
	260 265 270
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat	864
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His	
	275 280 285
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca	912
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr	
	290 295 300
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att	960
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile	
	305 310 315 320
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga	1008
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly	
	325 330 335

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```

gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa 1056
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys
      340              345              350

aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag 1104
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu
      355              360              365

ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa 1152
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys
      370              375              380

gag atg ctt gct aat tca gtt aaa gag ctt ac 1184
Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385              390

```

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<210> 66
<211> 394
<212> PRT
<213> ospC Chimera

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<400> 66
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1              5              10              15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20              25              30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35              40              45

Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50              55              60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
      65              70              75              80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
      85              90              95
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
      100              105              110
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
      115              120              125
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
      130              135              140
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
      145              150              155              160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
      165              170              175

```

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021005

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Concord, Massachusetts 01742-9133

Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
 180 185 190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
 195 200 205  
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
 210 215 220  
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
 225 230 235 240  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
 245 250 255  
 Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
 260 265 270  
 Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His  
 275 280 285  
 Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr  
 290 295 300  
 Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile  
 305 310 315 320  
 Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly  
 325 330 335  
 Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys  
 340 345 350  
 Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu  
 355 360 365  
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys  
 370 375 380  
 Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
 385 390

<210> 67  
 <211> 1184  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1184)

<400> 67  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
65 70 75 80	
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn	
85 90 95	
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100 105 110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115 120 125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130 135 140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145 150 155 160	
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165 170 175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	

7,060,281 B1

021005

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```

agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct 672
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser
210 215 220

aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa 768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
245 250 255

gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att 816
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
260 265 270

ggg aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac 864
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn
275 280 285

aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa 912
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu
290 295 300

aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca 960
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr
305 310 315 320

gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat 1008
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His
325 330 335

gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct 1056
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala
340 345 350

att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa 1104
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu
355 360 365

aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca 1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr
370 375 380

tta aaa aat gct gtt aaa gag ctt aca agt cc 1184
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
385 390

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7,060,281 B1

021005

Hamilton, Brook, Smith & Reynolds, P.C.  
530 Virginia Road, P.O. Box 9133  
Concord, Massachusetts 01742-9133

<210> 68  
 <211> 394  
 <212> PRT  
 <213> ospC Chimera

<400> 68  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
   1                  5                  10                  15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
           20                  25                  30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
           35                  40                  45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
   50                  55                  60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65                  70                  75                  80  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
           85                  90                  95  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
           100                  105                  110  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
           115                  120                  125  
 Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
   130                  135                  140  
  
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
 145                  150                  155                  160  
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
           165                  170                  175  
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
           180                  185                  190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
           195                  200                  205  
 Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser  
   210                  215                  220  
 Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
 225                  230                  235                  240  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
           245                  250                  255  
 Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
           260                  265                  270  
 Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn  
           275                  280                  285  
 Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu  
   290                  295                  300

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021005

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```

Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr
305                      310                      315                      320
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His
                      325                      330                      335
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala
                      340                      345                      350
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu
                      355                      360                      365
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr
                      370                      375                      380
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
385                      390

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<210> 69

<211> 1209

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1209)

<400> 69

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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1                      5                      10                      15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa      96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
                20                      25                      30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct     144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
                35                      40                      45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta     192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
                50                      55                      60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt     240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
        65                      70                      75                      80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat     288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
                85                      90                      95

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7,060,281 B1

021005

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 Concord, Massachusetts 01742-9133

```

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195 200 205

agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act 672
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
210 215 220

aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa 720
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
225 230 235 240

aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag 768
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
245 250 255

gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 816
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
260 265 270

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7,060,281 B1

021005

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Concord, Massachusetts 01742-9133

```

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 864
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
      275                      280                      285

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 912
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
      290                      295                      300

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 960
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
      305                      310                      315                      320

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 1008
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
      325                      330                      335

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1056
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
      340                      345                      350

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1104
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
      355                      360                      365

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1152
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
      370                      375                      380

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1200
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
      385                      390                      395                      400

aaa cct taa 1209
Lys Pro *
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<210> 70
<211> 402
<212> PRT
<213> ospC Chimera
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<400> 70
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1           5           10           15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20                      25                      30
```

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021005  
Hamilton, Brook, Smith & Reynolds, P.C.  
530 Virginia Road, P.O. Box 9133  
Concord, Massachusetts 01742-9133

```

Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35              40              45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50              55              60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
      65              70              75              80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
      85              90              95
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
      100             105             110
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
      115             120             125
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
      130             135             140
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
      145             150             155             160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
      165             170             175
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
      180             185             190
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
      195             200             205
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
      210             215             220
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
      225             230             235             240
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
      245             250             255
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
      260             265             270
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
      275             280             285
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
      290             295             300
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
      305             310             315             320
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
      325             330             335
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
      340             345             350
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
      355             360             365
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
      370             375             380
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
      385             390             395             400
Lys Pro

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 Concord, Massachusetts 01742-9133

<210> 71  
 <211> 1179  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1179)

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<400> 71
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1             5             10             15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa   96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
          20             25             30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct   144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
          35             40             45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt   192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
          50             55             60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt   240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
          65             70             75             80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc   288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
          85             90             95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct   336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
          100             105             110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag   384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
          115             120             125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa   432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
          130             135             140

```

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cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	
att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat	672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn	
210 215 220	
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu	
245 250 255	
act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa	816
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys	
260 265 270	
ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca	864
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser	
275 280 285	
tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata	912
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile	
290 295 300	
agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct	960
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala	
305 310 315 320	
aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca	1008
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr	
325 330 335	

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```

gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att 1056
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile
      340                      345                      350

tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag 1104
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys
      355                      360                      365

tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt 1152
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu
      370                      375                      380

act aat tca gtt aaa gag ctt aca agc 1179
Thr Asn Ser Val Lys Glu Leu Thr Ser
385                      390

```

```

<210> 72
<211> 393
<212> PRT
<213> ospC Chimera

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<400> 72
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1          5          10          15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20          25          30
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35          40          45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
      50          55          60
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65          70          75          80
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
      85          90          95
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
      100         105         110
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
      115         120         125
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
      130         135         140
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
145         150         155         160
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
      165         170         175

```

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Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
                   180                  185                  190  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
                   195                  200                  205  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
                   210                  215                  220  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
                   225                  230                  235                  240  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
                   245                  250                  255  
 Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys  
                   260                  265                  270  
 Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser  
                   275                  280                  285  
 Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile  
                   290                  295                  300  
 Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala  
                   305                  310                  315                  320  
 Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr  
                   325                  330                  335  
  
 Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile  
                   340                  345                  350  
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys  
                   355                  360                  365  
 Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu  
                   370                  375                  380  
 Thr Asn Ser Val Lys Glu Leu Thr Ser  
                   385                  390

<210> 73  
 <211> 1178  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1178)

<400> 73  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
   1                  5                  10                  15

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021005  
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 530 Virginia Road, P.O. Box 9133  
 Concord, Massachusetts 01742-9133



gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val	
50 55 60	
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt	240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu	
65 70 75 80	
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala	
85 90 95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	
100 105 110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	
115 120 125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	
130 135 140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	

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021005

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```

att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat 672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
210 215 220

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa 768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu
245 250 255

act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa 816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
260 265 270

aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga 864
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly
275 280 285

aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa 912
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys
290 295 300

tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat 960
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn
305 310 315 320

gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat 1008
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His
325 330 335

gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct 1056
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala
340 345 350

att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa 1104
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu
355 360 365

aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg 1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met
370 375 380

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021005

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Concord, Massachusetts 01742-9133

ctt gct aat tca gtt aaa gag ctt ac  
 Leu Ala Asn Ser Val Lys Glu Leu  
 385 390

1178

<210> 74  
 <211> 392  
 <212> PRT  
 <213> ospC Chimera

<400> 74  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 65 70 75 80  
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
 85 90 95  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
 100 105 110  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
 115 120 125  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
 130 135 140  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
 145 150 155 160  
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
 165 170 175  
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
 180 185 190  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
 195 200 205  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
 210 215 220  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
 225 230 235 240  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu  
 245 250 255  
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
 260 265 270

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Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly  
           275                          280                          285  
 Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys  
           290                          295                          300  
 Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn  
 305                          310                          315                          320  
 Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His  
                           325                          330                          335  
 Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala  
                           340                          345                          350  
 Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu  
           355                          360                          365  
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met  
           370                          375                          380  
 Leu Ala Asn Ser Val Lys Glu Leu  
 385                          390

<210> 75  
 <211> 1178  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1178)

<400> 75  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
   1                          5                          10                          15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
           20                          25                          30  
  
 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
           35                          40                          45  
  
 aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
           50                          55                          60  
  
 ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
   65                          70                          75                          80

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 Concord, Massachusetts 01742-9133

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala	
85 90 95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	
100 105 110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	
115 120 125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	
130 135 140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat	672
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn	
210 215 220	
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu	
245 250 255	

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```

acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag 816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
      260                265                270

aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca 864
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser
      275                280                285

ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta 912
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu
      290                295                300

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag 960
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
305                310                315                320

caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg 1008
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
      325                330                335

ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta 1056
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
      340                345                350

aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta 1104
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
      355                360                365

ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa 1152
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
      370                375                380

aat gct gtt aaa gag ctt aca agt cc 1178
Asn Ala Val Lys Glu Leu Thr Ser
385                390

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<210> 76

<211> 392

<212> PRT

<213> ospC Chimera

<400> 76

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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1              5              10              15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20                25                30

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021005

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Concord, Massachusetts 01742-9133

```

Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
    35              40              45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
    50              55              60
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
    65              70              75              80

Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
    85              90              95
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
    100             105             110
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
    115             120             125
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
    130             135             140
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
    145             150             155             160
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
    165             170             175
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
    180             185             190
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
    195             200             205
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn
    210             215             220
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
    225             230             235             240
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
    245             250             255
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
    260             265             270
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser
    275             280             285
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu
    290             295             300
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
    305             310             315             320
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
    325             330             335
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
    340             345             350
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
    355             360             365
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
    370             375             380
Asn Ala Val Lys Glu Leu Thr Ser
    385             390

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 Concord, Massachusetts 01742-9133

<210> 77  
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 <212> DNA  
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gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432

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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca	672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser	
210 215 220	
ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct	720
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro	
225 230 235 240	
aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta	768
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu	
245 250 255	
ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt	816
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
260 265 270	
tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac	864
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn	
275 280 285	
gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca	912
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser	
290 295 300	
aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag	960
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys	
305 310 315 320	

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aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag 1008
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys
325 330 335

cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat 1056
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp
340 345 350

aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt 1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly
355 360 365

gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa 1152
Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys
370 375 380

gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct 1200
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro
385 390 395 400

gtt gtg gca gaa agt cca aaa aaa cct taa 1230
Val Val Ala Glu Ser Pro Lys Lys Pro *
405

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<210> 78
<211> 409
<212> PRT
<213> ospC Chimera

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20 25 30
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35 40 45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100 105 110
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115 120 125

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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser  
 210 215 220  
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro  
 225 230 235 240  
 Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu  
 245 250 255  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 260 265 270  
 Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn  
 275 280 285  
 Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser  
 290 295 300  
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys  
 305 310 315 320  
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys  
 325 330 335  
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp  
 340 345 350  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly  
 355 360 365  
 Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys  
 370 375 380  
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro  
 385 390 395 400  
 Val Val Ala Glu Ser Pro Lys Lys Pro  
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<210> 79  
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 <212> DNA  
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<400> 79
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576

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Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser		
			180					185					190				
aaa	gca	gct	aaa	gag	atg	ctt	gct	aat	tca	ggt	aaa	gag	ctt	aca	agc	624	
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser		
			195				200					205					
cct	ggt	gtg	gca	gaa	agt	cca	aaa	aaa	cct	tcc	atg	gta	aat	aat	tca	672	
Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	Ser	Met	Val	Asn	Asn	Ser		
			210				215				220						
ggg	aaa	gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	ggt	aaa	720	
Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys		
225					230				235					240			
ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	gca	768	
Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala		
				245					250					255			
ggt	ggt	ctc	gcc	gtg	aaa	gaa	ggt	gaa	act	ttg	ctt	aca	tct	ata	gat	816	
Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Thr	Ser	Ile	Asp		
			260					265						270			
gag	ctt	gct	aaa	gct	att	ggt	aaa	aaa	ata	aaa	aac	gat	ggt	agt	tta	864	
Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Val	Ser	Leu		
			275				280					285					
gat	aat	gag	gca	gat	cac	aac	gga	tca	tta	ata	tca	gga	gca	tat	tta	912	
Asp	Asn	Glu	Ala	Asp	His	Asn	Gly	Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu		
			290				295				300						
att	tca	aac	tta	ata	aca	aaa	aaa	ata	agt	gca	ata	aaa	gat	tca	gga	960	
Ile	Ser	Asn	Leu	Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly		
305					310					315				320			
gaa	ttg	aag	gca	gaa	att	gaa	aag	gct	aag	aaa	tgt	tct	gaa	gaa	ttt	1008	
Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe		
				325				330						335			
act	gct	aaa	tta	aaa	ggt	gaa	cac	aca	gat	ctt	ggt	aaa	gaa	ggc	ggt	1056	
Thr	Ala	Lys	Leu	Lys	Gly	Glu	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val		
			340					345					350				
act	gat	gat	aat	gca	aaa	aaa	gcc	att	tta	aaa	aca	aat	aat	gat	aaa	1104	
Thr	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys		
			355				360					365					

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act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac 1152
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
    370                375                380

ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt 1200
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
    385                390                395                400

aca agc taa 1209
Thr Ser *
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<211> 402
<212> PRT
<213> ospC Chimera
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 20      25      30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35      40      45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50      55      60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65      70      75      80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85      90      95
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100     105     110
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115     120     125
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
130     135     140
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145     150     155     160
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
165     170     175
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
180     185     190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195     200     205
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
210     215     220
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Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
 225 230 235 240  
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala  
 245 250 255  
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp  
 260 265 270  
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu  
 275 280 285  
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu  
 290 295 300  
 Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly  
 305 310 315 320  
 Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe  
 325 330 335  
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val  
 340 345 350  
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys  
 355 360 365  
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn  
 370 375 380  
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu  
 385 390 395 400  
 Thr Ser

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 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45

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aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65 70 75 80	
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp	
85 90 95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100 105 110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115 120 125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca	672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser	
210 215 220	
gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa	720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys	
225 230 235 240	

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ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca	768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala	
245 250 255	
ggt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat	816
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp	
260 265 270	
gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt	864
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly	
275 280 285	
tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat	912
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr	
290 295 300	
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca	960
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser	
305 310 315 320	
gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat	1008
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp	
325 330 335	
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat	1056
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn	
340 345 350	
ggt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct	1104
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala	
355 360 365	
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa	1152
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu	
370 375 380	
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag	1200
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu	
385 390 395 400	
ctt ac	1205
Leu	

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 Concord, Massachusetts 01742-9133

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 <211> 401  
 <212> PRT  
 <213> ospC Chimera

<400> 82

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Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys
			20					25					30		
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro
		35					40					45			
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu
	50					55				60					
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile
65					70					75				80	
Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp
				85					90					95	
Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile
			100					105						110	
Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu
		115					120					125			
Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn
	130					135					140				
Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp
145					150					155				160	
Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys	Thr	Asn	Gly	Thr	Lys	Thr	Lys
				165					170					175	
Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser
			180				185						190		
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser
		195					200					205			
Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	Ser	Met	Val	Asn	Asn	Ser
		210					215				220				
Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys
225					230					235				240	
Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala
				245					250					255	
Val	Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp
			260					265					270		
Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly
		275					280						285		
Leu	Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr
		290				295					300				
Thr	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser
305					310					315				320	

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Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
      325              330              335
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
      340              345              350
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
      355              360              365
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
      370              375              380
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
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Leu

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  1              5              10              15

gca caa aaa ggt gct gag tca att gga tcc tgt agt aat tca ggg aaa      96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys
      20              25              30

ggt ggg gat tct gca tct act aat cct gct gac gag tct gcg aaa ggg      144
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly
      35              40              45

cct aat ctt aca gaa ata agc aaa aaa att aca gat tct aat gca ttt      192
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
      50              55              60

gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa      240
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
      65              70              75              80

ctt gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta      288
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
      85              90              95

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gct gct tta aat aat cag aat gga tgc ttg tta gca gga gcc tat gca 336
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala
      100                      105                      110

ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa 384
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu
      115                      120                      125

gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt 432
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe
      130                      135                      140

act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct 480
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala
      145                      150                      155                      160

acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc 528
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr
      165                      170                      175

gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt 576
Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly
      180                      185                      190

ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt 624
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu
      195                      200                      205

aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat 672
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn
      210                      215                      220

aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa 720
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys
      225                      230                      235                      240

gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca 768
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala
      245                      250                      255

ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat 816
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp
      260                      265                      270

gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta 864
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu
      275                      280                      285

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```

gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa 912
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu
290 295 300

ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa 960
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu
305 310 315 320

tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act 1008
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr
325 330 335

act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag 1056
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln
340 345 350

gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac 1104
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp
355 360 365

aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg 1152
Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu
370 375 380

tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca 1200
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
385 390 395 400

aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 1236
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<212> PRT
<213> ospC Chimera

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20 25 30
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly
35 40 45

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Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
  50                      55                      60
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
65                      70                      75                      80
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
                      85                      90                      95
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala
                      100                      105                      110
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu
                      115                      120                      125
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe
                      130                      135                      140
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala
145                      150                      155                      160
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr
                      165                      170                      175
Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly
                      180                      185                      190
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu
                      195                      200                      205
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn
210                      215                      220
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys
225                      230                      235                      240
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala
                      245                      250                      255
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp
                      260                      265                      270
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu
                      275                      280                      285
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu
290                      295                      300
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu
305                      310                      315                      320
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr
                      325                      330                      335
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln
                      340                      345                      350
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp
                      355                      360                      365
Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu
370                      375                      380
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
385                      390                      395                      400

Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
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 <211> 192  
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 <213> borrelia burgdorferi

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 20 25 30  
 Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu  
 35 40 45  
 Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn  
 50 55 60  
 Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser  
 65 70 75 80  
 Gly Ala Tyr Leu Ile Ser Thr Leu Ile Thr Lys Lys Ile Ser Ala Ile  
 85 90 95  
 Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys  
 100 105 110  
 Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly  
 115 120 125  
 Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr  
 130 135 140  
 Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu  
 145 150 155 160  
 Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser  
 165 170 175  
 Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
 180 185 190

<210> 86  
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 <213> borrelia burgdorferi

<400> 86  
 Asn Ser Gly Lys Gly Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser  
 1 5 10 15  
 Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser  
 20 25 30  
 Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser  
 35 40 45

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Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn
  50                      55                      60
Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly
65                      70                      75                      80
Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys
                      85                      90                      95
Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser
                      100                     105                     110
Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile
                      115                     120                     125
Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp
                      130                     135                     140
Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala
145                      150                      155                      160
Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val
                      165                      170                      175
Lys Glu Leu Thr Ser Pro Ile Val Ala Glu Ser Pro Lys Lys Pro
                      180                      185                      190

```

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# UNITED STATES PATENT AND TRADEMARK OFFICE

## CERTIFICATE OF CORRECTION

PATENT NO. : 7,060,281 B1  
 DATED : June 13, 2006  
 INVENTOR(S) : Raymond J. Dattwyler, Gerald Seinost, Daniel  
 Dykhuizen, Benjamin J. Luft, Maria J.C. Gomes-Solecki

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

**At Column 45, Insert SEQ ID NOS. 53-86 after SEQ ID NO: 52**

<210> 53

<211> 1137

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1137)

<400> 53

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1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192

MAILING ADDRESS OF SENDER:

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PATENT NO. 7,060,281 B1

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Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180 185 190

tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga 624  
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195 200 205

cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt 672  
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210 215 220

tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa 720  
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu  
225 230 235 240

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ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat	768
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp	
245 250 255	
aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata	816
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile	
260 265 270	
tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta	864
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu	
275 280 285	
aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act	912
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290 295 300	
aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat	960
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp	
305 310 315 320	
gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag	1008
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys	
325 330 335	
ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca	1056
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340 345 350	
aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat	1104
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn	
355 360 365	
cct gtt gtg gca gaa agt cca aaa aaa cct taa	1137
Pro Val Val Ala Glu Ser Pro Lys Lys Pro *	
370 375	

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 35 40 45  
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
 50 55 60  
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
 65 70 75 80  
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
 85 90 95  
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys  
 100 105 110  
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
 115 120 125  
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
 130 135 140  
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
 145 150 155 160  
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
 165 170 175  
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
 180 185 190  
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly  
 195 200 205  
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
 210 215 220  
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu  
 225 230 235 240  
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp  
 245 250 255  
 Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile  
 260 265 270  
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu  
 275 280 285  
 Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr  
 290 295 300  
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp  
 305 310 315 320

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Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
          325                      330                      335
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
          340                      345                      350
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
          355                      360                      365
Pro Val Val Ala Glu Ser Pro Lys Lys Pro
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<222> (1)...(1158)

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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa      96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
          20                      25                      30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg      144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
          35                      40                      45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa      192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
          50                      55                      60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca      240
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          65                      70                      75                      80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta      288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
          85                      90                      95

```

7,060,281 B1

021005  
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Concord, Massachusetts 01742-9133

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
180 185 190	
aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat	624
Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn	
195 200 205	
cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa	672
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys	
210 215 220	
att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct	720
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala	
225 230 235 240	
ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata	768
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile	
245 250 255	
aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg	816
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
260 265 270	
ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt	864
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser	
275 280 285	

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```

gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat 912
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
290 295 300

tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt 960
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
305 310 315 320

ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa 1008
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
325 330 335

aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt 1056
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
340 345 350

aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat 1104
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
355 360 365

tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa 1152
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
370 375 380

cct taa 1158
Pro *
385

```

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<210> 56
<211> 385
<212> PRT
<213> ospC Chimera

```

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<400> 56
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80

```

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021005  
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```

Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
      85                      90                      95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
      100                    105                    110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
      115                    120                    125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
      130                    135                    140
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145      150                    155                    160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
      165                    170                    175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
      180                    185                    190
Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
      195                    200                    205
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
      210                    215                    220
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
225      230                    235                    240
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile
      245                    250                    255
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
      260                    265                    270
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
      275                    280                    285
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
      290                    295                    300
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
305      310                    315                    320
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
      325                    330                    335
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
      340                    345                    350
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
      355                    360                    365
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
      370                    375                    380

```

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021005

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 Concord, Massachusetts 01742-9133



Pro  
385

<210> 57  
<211> 1161  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1161)

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<400> 57
atg tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct      48
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
  1              5              10              15

gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa      96
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
      20              25              30

att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act     144
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
      35              40              45

ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa     192
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
      50              55              60

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg     240
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
      65              70              75              80

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg     288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
      85              90              95

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct     336
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
      100             105             110

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca     384
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
      115             120             125

gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att     432

```

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021005  
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Asp	Leu	Gly	Lys	Gln	Asp	Ala	Thr	Asp	Asp	His	Ala	Lys	Ala	Ala	Ile	
130						135					140					
tta	aaa	aca	cat	gca	act	acc	gat	aaa	ggt	gct	aaa	gaa	ttt	aaa	gat	480
Leu	Lys	Thr	His	Ala	Thr	Thr	Asp	Lys	Gly	Ala	Lys	Glu	Phe	Lys	Asp	
145					150				155					160		
tta	ttt	gaa	tca	gta	gaa	ggt	ttg	tta	aaa	gca	gct	caa	gta	gca	cta	528
Leu	Phe	Glu	Ser	Val	Glu	Gly	Leu	Lys	Ala	Ala	Gln	Val	Ala	Leu		
				165				170					175			
act	aat	tca	ggt	aaa	gaa	ctt	aca	agt	cct	ggt	gta	gca	gaa	agt	cca	576
Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	
			180					185					190			
aaa	aaa	cct	cat	atg	gct	aat	aat	tca	ggt	ggg	gat	tct	gca	tct	act	624
Lys	Lys	Pro	His	Met	Ala	Asn	Asn	Ser	Gly	Gly	Asp	Ser	Ala	Ser	Thr	
		195					200				205					
aat	cct	gat	gag	tct	gca	aaa	gga	cct	aat	ctt	acc	gta	ata	agc	aaa	672
Asn	Pro	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Val	Ile	Ser	Lys	
	210					215				220						
aaa	att	aca	gat	tct	aat	gca	ttt	tta	ctg	gct	gtg	aaa	gaa	ggt	gag	720
Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	
225					230				235					240		
gct	ttg	ctt	tca	tct	ata	gat	gaa	ctt	tct	aaa	gct	att	ggt	aaa	aaa	768
Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ser	Lys	Ala	Ile	Gly	Lys	Lys	
				245				250						255		
ata	aaa	aat	gat	ggt	act	tta	gat	aac	gaa	gca	aat	cga	aac	gaa	tca	816
Ile	Lys	Asn	Asp	Gly	Thr	Leu	Asp	Asn	Glu	Ala	Asn	Arg	Asn	Glu	Ser	
			260					265					270			
ttg	ata	gca	gga	gct	tat	gaa	ata	tca	aaa	cta	ata	aca	caa	aaa	tta	864
Leu	Ile	Ala	Gly	Ala	Tyr	Glu	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	
		275					280					285				
agt	gta	ttg	aat	tca	gaa	gaa	tta	aag	aaa	aaa	att	aaa	gag	gct	aag	912
Ser	Val	Leu	Asn	Ser	Glu	Glu	Leu	Lys	Lys	Lys	Ile	Lys	Glu	Ala	Lys	
	290					295					300					
gat	tgt	tcc	caa	aaa	ttt	act	act	aag	cta	aaa	gat	agt	cat	gca	gag	960
Asp	Cys	Ser	Gln	Lys	Phe	Thr	Thr	Lys	Leu	Lys	Asp	Ser	His	Ala	Glu	
305				310					315						320	

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021005

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```

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1008
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
      325              330              335

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1056
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
      340              345              350

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1104
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
      355              360              365

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1152
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
      370              375              380

aaa cct taa 1161
Lys Pro *
385

```

```

<210> 58
<211> 386
<212> PRT
<213> ospC Chimera

```

```

<400> 58
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
 1      5      10      15
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
      20      25      30
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
      35      40      45
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
      50      55      60
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
      65      70      75      80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
      85      90      95
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
      100      105      110
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
      115      120      125
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
      130      135      140

```

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021005  
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Concord, Massachusetts 01742-9133

```

Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
145                      150                      155                      160
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
                      165                      170                      175
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
                      180                      185                      190
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
                      195                      200                      205
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
                      210                      215                      220
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
225                      230                      235                      240
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
                      245                      250                      255
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
                      260                      265                      270
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
                      275                      280                      285
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
                      290                      295                      300
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
305                      310                      315                      320
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
                      325                      330                      335
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
                      340                      345                      350
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
                      355                      360                      365
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
                      370                      375                      380
Lys Pro
385

```

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021005  
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530 Virginia Road, P.O. Box 9133  
Concord, Massachusetts 01742-9133

<210> 59  
 <211> 1197  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1197)

<400> 59  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480

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Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp		
145					150				155						160		
gct	gat	gca	aaa	gaa	gcc	att	tta	aaa	aca	aat	ggt	act	aaa	act	aaa	528	
Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys	Thr	Asn	Gly	Thr	Lys	Thr	Lys		
			165					170					175				
ggt	gct	gaa	gaa	ctt	gga	aaa	tta	ttt	gaa	tca	gta	gag	gtc	ttg	tca	576	
Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser		
		180					185					190					
aaa	gca	gct	aaa	gag	atg	ctt	gct	aat	tca	ggt	aaa	gag	ctt	aca	agc	624	
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser		
		195				200					205						
cct	ggt	gtg	gca	gaa	agt	cca	gcc	atg	gta	aat	aat	tca	ggg	aaa	gat	672	
Pro	Val	Val	Ala	Glu	Ser	Pro	Ala	Met	Val	Asn	Asn	Ser	Gly	Lys	Asp		
	210					215					220						
ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	ggt	aaa	ggg	cct	aat	720	
Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn		
225				230					235					240			
ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	gca	ggt	ggt	ctc	768	
Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu		
			245					250						255			
gcc	gtg	aaa	gaa	ggt	gaa	act	ttg	ctt	aca	tct	ata	gat	gag	ctt	gct	816	
Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Thr	Ser	Ile	Asp	Glu	Leu	Ala		
			260				265						270				
aaa	gct	att	ggt	aaa	aaa	ata	aaa	aac	gat	ggt	agt	tta	gat	aat	gag	864	
Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Val	Ser	Leu	Asp	Asn	Glu		
		275				280						285					
gca	gat	cac	aac	gga	tca	tta	ata	tca	gga	gca	tat	tta	att	tca	aac	912	
Ala	Asp	His	Asn	Gly	Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn		
		290				295					300						
tta	ata	aca	aaa	aaa	ata	agt	gca	ata	aaa	gat	tca	gga	gaa	ttg	aag	960	
Leu	Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys		
305					310				315					320			
gca	gaa	att	gaa	aag	gct	aag	aaa	tgt	tct	gaa	gaa	ttt	act	gct	aaa	1008	
Ala	Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys		
			325					330						335			

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021005

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 Concord, Massachusetts 01742-9133

```

tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat      1056
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
      340                      345                      350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc      1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
      355                      360                      365

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa      1152
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
      370                      375                      380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc          1197
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
      385                      390                      395

```

```

<210> 60
<211> 399
<212> PRT
<213> ospC Chimera

```

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<400> 60
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1          5          10          15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20          25          30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35          40          45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50          55          60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
      65          70          75          80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
      85          90          95
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
      100         105         110
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
      115         120         125
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
      130         135         140
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
      145         150         155         160
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
      165         170         175
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
      180         185         190

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021005  
 Hamilton, Brook, Smith & Reynolds, P.C.  
 530 Virginia Road, P.O. Box 9133  
 Concord, Massachusetts 01742-9133

```

Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
    195                200                205
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
    210                215                220
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
    225                230                235                240

Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
    245                250                255
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala
    260                265                270
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu
    275                280                285
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn
    290                295                300
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys
    305                310                315                320
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys
    325                330                335
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
    340                345                350
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
    355                360                365
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
    370                375                380
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
    385                390                395

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<210> 61
<211> 1196
<212> DNA
<213> ospC Chimera

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<220>
<221> CDS
<222> (1)...(1196)

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<400> 61
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1                5                10                15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa   96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
    20                25                30

```

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65 70 75 80	
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp	
85 90 95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100 105 110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115 120 125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat	672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp	
210 215 220	

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```

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
225                230                235                240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg 768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
                245                250                255

gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct 816
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
                260                265                270

act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc 864
Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val
                275                280                285

gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca 912
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser
                290                295                300

aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta 960
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu
305                310                315                320

aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa 1008
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys
                325                330                335

aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat 1056
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp
                340                345                350

gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag 1104
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys
                355                360                365

ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca 1152
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala
                370                375                380

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac 1196
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385                390                395

```

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<210> 62  
 <211> 398  
 <212> PRT  
 <213> ospC Chimera

<400> 62  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
 210 215 220  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 225 230 235 240  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
 245 250 255  
 Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala  
 260 265 270  
 Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val  
 275 280 285  
 Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 290 295 300  
 Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu  
 305 310 315 320

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Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys  
 325 330 335

Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp  
 340 345 350  
 Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys  
 355 360 365  
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala  
 370 375 380  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
 385 390 395

<210> 63  
 <211> 1185  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1185)

<400> 63  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65 70 75 80  
 gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85 90 95

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100 105 110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115 120 125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130 135 140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145 150 155 160	
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165 170 175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	
agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser	
210 215 220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245 250 255	
gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt	816
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly	
260 265 270	
aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac	864

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```

Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn
    275                      280                      285

gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa    912
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys
    290                      295                      300

aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa    960
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu
    305                      310                      315                      320

aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa    1008
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu
    325                      330                      335

cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa    1056
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys
    340                      345                      350

gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt    1104
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu
    355                      360                      365

gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag    1152
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu
    370                      375                      380

atg ctt act aat tca gtt aaa gag ctt aca agc                            1185
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
    385                      390                      395

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<210> 64
<211> 395
<212> PRT
<213> ospC Chimera

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<400> 64
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1                      5                      10                      15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
    20                      25                      30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
    35                      40                      45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
    50                      55                      60

```

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```

Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65          70          75          80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
          85          90          95
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
          100         105         110
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
          115         120         125
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
          130         135         140
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145          150         155         160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
          165         170         175
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
          180         185         190
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
          195         200         205
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
          210         215         220
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225          230         235         240
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
          245         250         255
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly
          260         265         270
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn
          275         280         285
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys
          290         295         300
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu
305          310         315         320
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu
          325         330         335
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys
          340         345         350
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu
          355         360         365
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu
          370         375         380
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
385          390         395

```

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<210> 65  
 <211> 1184  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1184)

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<400> 65
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1             5             10             15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa   96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
          20             25             30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct  144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
          35             40             45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta  192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
          50             55             60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt  240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
          65             70             75             80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat  288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
          85             90             95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca  336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
          100             105             110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta  384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
          115             120             125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act  432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
          130             135             140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat  480

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Lys	Leu	Lys	Asp	Asn	His	Ala	Gln	Leu	Gly	Ile	Gln	Gly	Val	Thr	Asp		
145					150					155					160		
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528																	
Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Ala	Asn	Ala	Ala	Gly	Lys	Asp		
				165					170					175			
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576																	
Lys	Gly	Val	Glu	Glu	Leu	Glu	Lys	Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu		
			180					185					190				
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624																	
Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr		
		195					200					205					
agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct 672																	
Ser	Pro	Val	Val	His	Gly	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser		
		210				215					220						
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720																	
Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile		
225					230					235					240		
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa 768																	
Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu		
			245						250					255			
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att 816																	
Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile		
			260					265					270				
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat 864																	
Gly	Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	Leu	Ala	Val	Glu	Ala	Gly	His		
		275					280					285					
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca 912																	
Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser	Lys	Leu	Ile	Thr		
		290				295					300						
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att 960																	
Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	Glu	Lys	Leu	Lys	Glu	Lys	Ile		
305					310					315					320		
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga 1008																	
Glu	Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe	Thr	Lys	Lys	Leu	Glu	Gly		
				325				330						335			

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```

gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa 1056
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys
      340              345              350

aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag 1104
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu
      355              360              365

ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa 1152
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys
      370              375              380

gag atg ctt gct aat tca gtt aaa gag ctt ac 1184
Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385              390

```

```

<210> 66
<211> 394
<212> PRT
<213> ospC Chimera

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<400> 66
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1          5          10          15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20          25          30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35          40          45

Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50          55          60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65          70          75          80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
      85          90          95
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
      100          105          110
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
      115          120          125
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
      130          135          140
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145          150          155          160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
      165          170          175

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Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
 180 185 190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
 195 200 205  
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
 210 215 220  
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
 225 230 235 240  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
 245 250 255  
 Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
 260 265 270  
 Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His  
 275 280 285  
 Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr  
 290 295 300  
 Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile  
 305 310 315 320  
 Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly  
 325 330 335  
 Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys  
 340 345 350  
 Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu  
 355 360 365  
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys  
 370 375 380  
 Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
 385 390

<210> 67  
 <211> 1184  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1184)

<400> 67  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30

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021005  
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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
65 70 75 80	
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn	
85 90 95	
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100 105 110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115 120 125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130 135 140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145 150 155 160	
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165 170 175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	

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agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser	
210 215 220	
aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245 250 255	
gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att	816
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile	
260 265 270	
ggg aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac	864
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn	
275 280 285	
aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa	912
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu	
290 295 300	
aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca	960
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr	
305 310 315 320	
gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat	1008
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His	
325 330 335	
gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct	1056
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala	
340 345 350	
att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa	1104
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355 360 365	
aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr	
370 375 380	
tta aaa aat gct gtt aaa gag ctt aca agt cc	1184
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser	
385 390	

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<210> 68  
 <211> 394  
 <212> PRT  
 <213> ospC Chimera

<400> 68  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
   1                  5                  10                  15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
           20                  25                  30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
           35                  40                  45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
           50                  55                  60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
   65                  70                  75                  80  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
           85                  90                  95  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
           100                  105                  110  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
           115                  120                  125  
 Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
           130                  135                  140  
  
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
   145                  150                  155                  160  
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
           165                  170                  175  
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
           180                  185                  190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
           195                  200                  205  
 Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser  
           210                  215                  220  
 Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
   225                  230                  235                  240  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
           245                  250                  255  
 Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
           260                  265                  270  
 Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn  
           275                  280                  285  
 Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu  
           290                  295                  300

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```

Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr
305          310          315          320
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His
          325          330          335
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala
          340          345          350
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu
          355          360          365
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr
          370          375          380
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
385          390

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<210> 69
<211> 1209
<212> DNA
<213> ospC Chimera

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<220>
<221> CDS
<222> (1)...(1209)

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<400> 69
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt      48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1          5          10          15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa      96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
          20          25          30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct     144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
          35          40          45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta     192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
          50          55          60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt     240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
          65          70          75          80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat     288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
          85          90          95

```

7,060,281 B1

021005  
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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100 105 110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115 120 125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130 135 140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145 150 155 160	
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165 170 175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	
agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
210 215 220	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	720
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
225 230 235 240	
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	768
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
245 250 255	
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa	816
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys	
260 265 270	

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021005

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```

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca      864
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
      275                      280                      285

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta      912
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
      290                      295                      300

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag      960
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
      305                      310                      315                      320

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag      1008
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
      325                      330                      335

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta      1056
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
      340                      345                      350

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta      1104
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
      355                      360                      365

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act      1152
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
      370                      375                      380

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa      1200
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
      385                      390                      395                      400

aaa cct taa
Lys Pro *
      1209

```

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<210> 70
<211> 402
<212> PRT
<213> ospC Chimera

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```

<400> 70
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1           5           10           15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20                      25                      30

```

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021005  
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```

Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35              40              45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50              55              60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
      65              70              75              80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
      85              90              95
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
      100             105             110
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
      115             120             125
Lys Glu Lys Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
      130             135             140
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
      145             150             155             160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
      165             170             175
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
      180             185             190
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
      195             200             205
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
      210             215             220
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
      225             230             235             240
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
      245             250             255
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
      260             265             270
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
      275             280             285
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
      290             295             300
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
      305             310             315             320
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
      325             330             335
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
      340             345             350
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
      355             360             365
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
      370             375             380
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
      385             390             395             400
Lys Pro

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021005

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Concord, Massachusetts 01742-9133

<210> 71  
 <211> 1179  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1179)

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<400> 71
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1             5             10             15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa   96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
          20             25             30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct   144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
          35             40             45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt   192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
          50             55             60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt   240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
          65             70             75             80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc   288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
          85             90             95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct   336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
          100            105            110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag   384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
          115            120            125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa   432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
          130            135            140

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021005  
 Hamilton, Brook, Smith & Reynolds, P.C.  
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 Concord, Massachusetts 01742-9133

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	
att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat	672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn	
210 215 220	
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu	
245 250 255	
act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa	816
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys	
260 265 270	
ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca	864
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser	
275 280 285	
tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata	912
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile	
290 295 300	
agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct	960
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala	
305 310 315 320	
aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca	1008
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr	
325 330 335	

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021005

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 530 Virginia Road, P.O. Box 9133  
 Concord, Massachusetts 01742-9133

```

gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att 1056
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile
      340                      345                      350

tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag 1104
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys
      355                      360                      365

tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt 1152
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu
      370                      375                      380

act aat tca gtt aaa gag ctt aca agc 1179
Thr Asn Ser Val Lys Glu Leu Thr Ser
385                      390

```

```

<210> 72
<211> 393
<212> PRT
<213> ospC Chimera

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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
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      20          25          30
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35          40          45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
      50          55          60
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65          70          75          80
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
      85          90          95
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
      100          105          110
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
      115          120          125
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
      130          135          140
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
145          150          155          160
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
      165          170          175

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Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
                   180                  185                  190  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
                   195                  200                  205  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
                   210                  215                  220  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
                   225                  230                  235                  240  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
                   245                  250                  255  
 Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys  
                   260                  265                  270  
 Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser  
                   275                  280                  285  
 Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile  
                   290                  295                  300  
 Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala  
                   305                  310                  315                  320  
 Lys Lys Cys Ser Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr  
                   325                  330                  335  
  
 Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile  
                   340                  345                  350  
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys  
                   355                  360                  365  
 Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu  
                   370                  375                  380  
 Thr Asn Ser Val Lys Glu Leu Thr Ser  
                   385                  390

<210> 73  
 <211> 1178  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1178)

<400> 73  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
   1                  5                  10                  15

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gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val	
50 55 60	
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt	240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu	
65 70 75 80	
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala	
85 90 95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	
100 105 110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	
115 120 125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	
130 135 140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	

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att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat	672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn	
210 215 220	
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu	
245 250 255	
act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa	816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys	
260 265 270	
aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga	864
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly	
275 280 285	
aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa	912
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys	
290 295 300	
tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn	
305 310 315 320	
gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His	
325 330 335	
gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala	
340 345 350	
att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355 360 365	
aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met	
370 375 380	

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ctt gct aat tca gtt aaa gag ctt ac  
 Leu Ala Asn Ser Val Lys Glu Leu  
 385 390

1178

<210> 74  
 <211> 392  
 <212> PRT  
 <213> ospC Chimera

<400> 74  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 65 70 75 80  
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
 85 90 95  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
 100 105 110  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
 115 120 125  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
 130 135 140  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
 145 150 155 160  
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
 165 170 175  
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
 180 185 190  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
 195 200 205  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
 210 215 220  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
 225 230 235 240  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu  
 245 250 255  
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
 260 265 270

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```

Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly
      275                      280                      285
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys
      290                      295                      300
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn
305                      310                      315                      320
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His
      325                      330                      335
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala
      340                      345                      350
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu
      355                      360                      365
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met
      370                      375                      380
Leu Ala Asn Ser Val Lys Glu Leu
385                      390

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<210> 75
<211> 1178
<212> DNA
<213> ospC Chimera

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<220>
<221> CDS
<222> (1)...(1178)

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<400> 75
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
  1                      5                      10                      15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa   96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20                      25                      30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct   144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35                      40                      45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt   192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
      50                      55                      60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt   240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
      65                      70                      75                      80

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gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala	
85 90 95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	
100 105 110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	
115 120 125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	
130 135 140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat	672
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn	
210 215 220	
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu	
245 250 255	

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```

acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag      816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
      260                      265                      270

aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca      864
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser
      275                      280                      285

ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta      912
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu
      290                      295                      300

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag      960
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
      305                      310                      315                      320

caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg      1008
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
      325                      330                      335

ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta      1056
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
      340                      345                      350

aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta      1104
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
      355                      360                      365

ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa      1152
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
      370                      375                      380

aat gct gtt aaa gag ctt aca agt cc                                  1178
Asn Ala Val Lys Glu Leu Thr Ser
      385                      390

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<210> 76

<211> 392

<212> PRT

<213> ospC Chimera

<400> 76

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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1                      5                      10                      15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20                      25                      30

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```

Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
    35              40              45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
    50              55              60
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
    65              70              75              80

Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
    85              90              95
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
    100             105             110
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
    115             120             125
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
    130             135             140
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
    145             150             155             160
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
    165             170             175
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
    180             185             190
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
    195             200             205
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn
    210             215             220
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
    225             230             235             240
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
    245             250             255
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
    260             265             270
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser
    275             280             285
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu
    290             295             300
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
    305             310             315             320
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
    325             330             335
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
    340             345             350
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
    355             360             365
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
    370             375             380
Asn Ala Val Lys Glu Leu Thr Ser
    385             390

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<210> 77  
 <211> 1230  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1230)

<400> 77  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432

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Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn		
130						135					140						
aaa	tta	aaa	gaa	aaa	cac	aca	gat	ctt	ggt	aaa	gaa	ggt	gtt	act	gat	480	
Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp		
145					150					155					160		
gct	gat	gca	aaa	gaa	gcc	att	tta	aaa	aca	aat	ggt	act	aaa	act	aaa	528	
Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys	Thr	Asn	Gly	Thr	Lys	Thr	Lys		
				165					170					175			
ggt	gct	gaa	gaa	ctt	gga	aaa	tta	ttt	gaa	tca	gta	gag	gtc	ttg	tca	576	
Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser		
		180						185					190				
aaa	gca	gct	aaa	gag	atg	ctt	gct	aat	tca	ggt	aaa	gag	ctt	aca	agc	624	
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser		
		195					200					205					
cct	ggt	gtg	gca	gaa	agt	cca	aaa	aaa	cct	ttc	cat	ggt	aat	aat	tca	672	
Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	Phe	His	Gly	Asn	Asn	Ser		
	210					215					220						
ggt	ggg	gat	tct	gca	tct	act	aat	cct	gat	gag	tct	gca	aaa	gga	cct	720	
Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	Asp	Glu	Ser	Ala	Lys	Gly	Pro		
225					230				235						240		
aat	ctt	acc	gta	ata	agc	aaa	aaa	att	aca	gat	tct	aat	gca	ttt	tta	768	
Asn	Leu	Thr	Val	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	Leu		
			245						250					255			
ctg	gct	gtg	aaa	gaa	gtt	gag	gct	ttg	ctt	tca	tct	ata	gat	gaa	ctt	816	
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu		
		260						265					270				
tct	aaa	gct	att	ggt	aaa	aaa	ata	aaa	aat	gat	ggt	act	tta	gat	aac	864	
Ser	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Thr	Leu	Asp	Asn		
		275					280					285					
gaa	gca	aat	cga	aac	gaa	tca	ttg	ata	gca	gga	gct	tat	gaa	ata	tca	912	
Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu	Ile	Ala	Gly	Ala	Tyr	Glu	Ile	Ser		
		290				295					300						
aaa	cta	ata	aca	caa	aaa	tta	agt	gta	ttg	aat	tca	gaa	gaa	tta	aag	960	
Lys	Leu	Ile	Thr	Gln	Lys	Leu	Ser	Val	Leu	Asn	Ser	Glu	Glu	Leu	Lys		
305					310					315					320		

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```

aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag 1008
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys
      325              330              335

cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat 1056
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp
      340              345              350

aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt 1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly
      355              360              365

gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa 1152
Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys
      370              375              380

gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct 1200
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro
      385              390              395              400

gtt gtg gca gaa agt cca aaa aaa cct taa 1230
Val Val Ala Glu Ser Pro Lys Lys Pro *
      405

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<210> 78
<211> 409
<212> PRT
<213> ospC Chimera

```

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<400> 78
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1          5          10          15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20          25          30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35          40          45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50          55          60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
      65          70          75          80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
      85          90          95
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
      100         105         110
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
      115         120         125

```

7,060,281 B1

021005  
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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
130                      135                      140

Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145                      150                      155                      160
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
165                      170                      175
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
180                      185                      190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195                      200                      205
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser
210                      215                      220
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro
225                      230                      235                      240
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu
245                      250                      255
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
260                      265                      270
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn
275                      280                      285
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser
290                      295                      300
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys
305                      310                      315                      320
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys
325                      330                      335
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp
340                      345                      350
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly
355                      360                      365
Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys
370                      375                      380
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro
385                      390                      395                      400
Val Val Ala Glu Ser Pro Lys Lys Pro
405

```

```

<210> 79
<211> 1209
<212> DNA
<213> ospC Chimera

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<220>
<221> CDS
<222> (1)...(1209)

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7,060,281 B1

021005  
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```

<400> 79
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt      48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1              5              10              15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa      96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
      20              25              30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct      144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
      35              40              45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta      192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50              55              60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att      240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
      65              70              75              80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat      288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
      85              90              95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata      336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
      100             105             110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta      384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
      115             120             125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat      432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
      130             135             140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat      480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
      145             150             155             160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa      528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
      165             170             175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca      576

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Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser		
			180					185					190				
aaa	gca	gct	aaa	gag	atg	ctt	gct	aat	tca	ggt	aaa	gag	ctt	aca	agc	624	
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser		
			195				200					205					
cct	ggt	gtg	gca	gaa	agt	cca	aaa	aaa	cct	tcc	atg	gta	aat	aat	tca	672	
Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	Ser	Met	Val	Asn	Asn	Ser		
			210				215				220						
ggg	aaa	gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	ggt	aaa	720	
Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys		
225					230					235					240		
ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	gca	768	
Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala		
				245					250					255			
gtt	gtt	ctc	gcc	gtg	aaa	gaa	gtt	gaa	act	ttg	ctt	aca	tct	ata	gat	816	
Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Thr	Ser	Ile	Asp		
			260					265					270				
gag	ctt	gct	aaa	gct	att	ggt	aaa	aaa	ata	aaa	aac	gat	ggt	agt	tta	864	
Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Val	Ser	Leu		
			275				280					285					
gat	aat	gag	gca	gat	cac	aac	gga	tca	tta	ata	tca	gga	gca	tat	tta	912	
Asp	Asn	Glu	Ala	Asp	His	Asn	Gly	Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu		
			290			295					300						
att	tca	aac	tta	ata	aca	aaa	aaa	ata	agt	gca	ata	aaa	gat	tca	gga	960	
Ile	Ser	Asn	Leu	Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly		
305					310					315					320		
gaa	ttg	aag	gca	gaa	att	gaa	aag	gct	aag	aaa	tgt	tct	gaa	gaa	ttt	1008	
Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe		
			325					330					335				
act	gct	aaa	tta	aaa	ggt	gaa	cac	aca	gat	ctt	ggt	aaa	gaa	ggc	gtt	1056	
Thr	Ala	Lys	Leu	Lys	Gly	Glu	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val		
			340					345					350				
act	gat	gat	aat	gca	aaa	aaa	gcc	att	tta	aaa	aca	aat	aat	gat	aaa	1104	
Thr	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys		
			355				360					365					

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act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac 1152  
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn  
 370 375 380

ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt 1200  
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu  
 385 390 395 400

aca agc taa 1209  
 Thr Ser \*

<210> 80  
 <211> 402  
 <212> PRT  
 <213> ospC Chimera

<400> 80  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser  
 210 215 220

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021005  
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Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
 225 230 235 240  
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala  
 245 250 255  
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp  
 260 265 270  
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu  
 275 280 285  
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu  
 290 295 300  
 Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly  
 305 310 315 320  
 Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe  
 325 330 335  
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val  
 340 345 350  
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys  
 355 360 365  
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn  
 370 375 380  
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu  
 385 390 395 400  
 Thr Ser

<210> 81  
 <211> 1205  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1205)

<400> 81  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45

7,060,281 B1

021005  
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```

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195 200 205

cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
210 215 220

gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
225 230 235 240

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ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca	768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala	
245 250 255	
gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat	816
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp	
260 265 270	
gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt	864
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly	
275 280 285	
tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat	912
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr	
290 295 300	
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca	960
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser	
305 310 315 320	
gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat	1008
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp	
325 330 335	
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat	1056
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn	
340 345 350	
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct	1104
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala	
355 360 365	
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa	1152
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu	
370 375 380	
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag	1200
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu	
385 390 395 400	
ctt ac	1205
Leu	

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021005

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<210> 82  
 <211> 401  
 <212> PRT  
 <213> ospC Chimera

<400> 82  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser  
 210 215 220  
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
 225 230 235 240  
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala  
 245 250 255  
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp  
 260 265 270  
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly  
 275 280 285  
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr  
 290 295 300  
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser  
 305 310 315 320

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```

Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
      325                      330          335
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
      340                      345          350
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
      355                      360          365
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
      370                      375          380
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
385                      390          395          400
Leu

```

```

<210> 83
<211> 1236
<212> DNA
<213> ospC Chimera

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<220>
<221> CDS
<222> (1)...(1236)

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<400> 83
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
  1                      5                      10          15

gca caa aaa ggt gct gag tca att gga tcc tgt agt aat tca ggg aaa   96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys
      20                      25          30

ggt ggg gat tct gca tct act aat cct gct gac gag tct gcg aaa ggg   144
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly
      35                      40          45

cct aat ctt aca gaa ata agc aaa aaa att aca gat tct aat gca ttt   192
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
      50                      55          60

gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa   240
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
      65                      70          75          80

ctt gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta   288
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
      85                      90          95

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gct gct tta aat aat cag aat gga tct ttg tta gca gga gcc tat gca	336
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala	
100 105 110	
ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa	384
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu	
115 120 125	
gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt	432
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe	
130 135 140	
act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct	480
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala	
145 150 155 160	
acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc	528
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr	
165 170 175	
gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt	576
Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly	
180 185 190	
ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt	624
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu	
195 200 205	
aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat	672
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn	
210 215 220	
aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa	720
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys	
225 230 235 240	
gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca	768
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala	
245 250 255	
ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat	816
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp	
260 265 270	
gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta	864
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu	
275 280 285	

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gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa 912
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu
290 295 300

ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa 960
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu
305 310 315 320

tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act 1008
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr
325 330 335

act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag 1056
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln
340 345 350

gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac 1104
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp
355 360 365

aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg 1152
Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu
370 375 380

tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca 1200
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
385 390 395 400

aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 1236
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
405 410

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<210> 84
<211> 411
<212> PRT
<213> ospC Chimera

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<400> 84
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys
20 25 30
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly
35 40 45

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Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
  50                      55                      60
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
65                      70                      75                      80
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
                      85                      90                      95
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala
  100                      105                      110
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu
  115                      120                      125
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe
  130                      135                      140
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala
145                      150                      155                      160
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr
                      165                      170                      175
Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly
  180                      185                      190
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu
  195                      200                      205
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn
  210                      215                      220
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys
225                      230                      235                      240
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala
  245                      250                      255
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp
  260                      265                      270
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu
  275                      280                      285
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu
  290                      295                      300
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu
305                      310                      315                      320
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr
  325                      330                      335
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln
  340                      345                      350
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp
  355                      360                      365
Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu
  370                      375                      380
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
385                      390                      395                      400

Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
      405                      410

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<210> 85  
 <211> 192  
 <212> PRT  
 <213> borrelia burgdorferi

<400> 85  
 Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp  
 1 5 10 15  
 Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr  
 20 25 30  
 Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu  
 35 40 45  
 Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn  
 50 55 60  
 Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser  
 65 70 75 80  
 Gly Ala Tyr Leu Ile Ser Thr Leu Ile Thr Lys Lys Ile Ser Ala Ile  
 85 90 95  
 Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys  
 100 105 110  
 Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly  
 115 120 125  
 Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr  
 130 135 140  
 Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu  
 145 150 155 160  
 Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser  
 165 170 175  
 Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
 180 185 190

<210> 86  
 <211> 191  
 <212> PRT  
 <213> borrelia burgdorferi

<400> 86  
 Asn Ser Gly Lys Gly Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser  
 1 5 10 15  
 Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser  
 20 25 30  
 Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser  
 35 40 45

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Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn
  50                      55                      60
Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly
  65                      70                      75                      80
Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys
                      85                      90                      95
Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser
      100                      105                      110
Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile
      115                      120                      125
Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp
      130                      135                      140
Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala
      145                      150                      155                      160
Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val
                      165                      170                      175
Lys Glu Leu Thr Ser Pro Ile Val Ala Glu Ser Pro Lys Lys Pro
      180                      185                      190

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